

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,491

DATE: 10/11/2001
TIME: 10:07:46

Input Set : A:\A68285.ST25.txt

Output Set: N:\CRF3\10112001\I762491.raw

ENTERED

OK

3 <110> APPLICANT: Luo, Ying
4 Huang, Betty
5 Shen, Mary
6 Yu, PeiWen
8 <120> TITLE OF INVENTION: NOVEL APOPTOSIS PROTEINS
10 <130> FILE REFERENCE: A-68285/RMS/DHR
12 <140> CURRENT APPLICATION NUMBER: US 09/762,491
13 <141> CURRENT FILING DATE: 2001-05-09
15 <150> PRIOR APPLICATION NUMBER: PCT/US. 99/17776
16 <151> PRIOR FILING DATE: 1999-08-06
18 <150> PRIOR APPLICATION NUMBER: US 60/099,486
19 <151> PRIOR FILING DATE: 1998-09-08
21 <150> PRIOR APPLICATION NUMBER: US 60/095,590
22 <151> PRIOR FILING DATE: 1998-08-06
24 <150> PRIOR APPLICATION NUMBER: US 60/095,587
25 <151> PRIOR FILING DATE: 1998-08-06
27 <160> NUMBER OF SEQ ID NOS: 10
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1155
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
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39 caaatccatg caaaggccgt ttaaaaaatag cagcgaaggt cctggactcg gtctcgtcca 120
41 gcacagcccc ttgctctct ctctgggctc tggcgcctg gccccgggg acccacacga 180
43 ggatcatggcg tgcttcgggc agggggggcgg ggtatccata gacacctcag ctcttaaga 240
45 gttctccgcc tgggccagga cgagcatggg ggtcccccact gatgcccgag acagtgcacc 300
47 tgtgtgtgtg agccctcgac ccacataaca gagagggtgtc ctgatgcct ctgtcctctc 360
49 caggtggatc taggatccgg cttccaacat gtggcagctc tgggcctccc tctgtgcct 420
51 gctggtgttg gccaatgccc ggagcaggcc ctctttccat cccgtgtcgg atgagctggt 480
53 caactatgtc aacaaacgga ataccacgtg gcaggccggg cacaacttct acaacgtgga 540
55 catgagctac ttgaagagga tatgtgtgtc cttcctgggt gggcccaagc caccacagag 600
57 agttatgttt accgaggacc tgaagctgcc tgcaagcttc gatgcacggg aacaatggcc 660
59 acagtgtccc accatcaaag agatcagaga ccagggtccc tgtggctcct gctgggtaag 720
61 gccctgctgg ctggtgggga agcgtctggag agaaagtggg agcaacactg gagagtcttg 780
63 ggggattcgg ggtggggaca actctgacaa ggcaagttaa agaaactttc tgagtccag 840
65 tttccatcag tacaaaaatc acaatccctc tggccatgaa tgatggcgag gattaggtgg 900
67 agtggcgggc agagcatcca gcagattgca agtccacgtg tacagggtggc gaagcagctc 960
69 cttttccctg acatgctggc ccgtccgcaa ataccaggag ctctcactgc tactctgctt 1020
71 caagaaagca tcccttagt gtcagtgagc tgtcttaatt ttgtcattta attgtggtaa 1080
73 aatacacgta acagaaatgt aataatctta gcaatcttct tttgttttct ttttctttt 1140
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78 <210> SEQ ID NO: 2
79 <211> LENGTH: 164
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens

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86 1 5 10 15
89 Ala Arg Ser Arg Pro Ser Phe His Pro Val Ser Asp Glu Leu Val Asn
90 20 25 30
93 Tyr Val Asn Lys Arg Asn Thr Thr Trp Gln Ala Gly His Asn Phe Tyr
94 35 40 45
97 Asn Val Asp Met Ser Tyr Leu Lys Arg Leu Cys Gly Thr Phe Leu Gly
98 50 55 60
101 Gly Pro Lys Pro Pro Gln Arg Val Met Phe Thr Glu Asp Leu Lys Leu
102 65 70 75 80
105 Pro Ala Ser Phe Asp Ala Arg Glu Gln Trp Pro Gln Cys Pro Thr Ile
106 85 90 95
109 Lys Glu Ile Arg Asp Gln Gly Ser Cys Gly Ser Cys Trp Val Arg Pro
110 100 105 110
113 Cys Trp Leu Val Gly Lys Arg Trp Arg Glu Ser Gly Ser Asn Thr Gly
114 115 120 125
117 Glu Ser Trp Gly Ile Arg Gly Gly Asp Asn Ser Asp Lys Ala Ser Tyr
118 130 135 140
121 Arg Asn Phe Leu Ser Pro Ser Phe His Gln Tyr Lys Asn His Asn Pro
122 145 150 155 160

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125 Ser Gly His Glu

129 <210> SEQ ID NO: 3

130 <211> LENGTH: 1294

131 <212> TYPE: DNA

132 <213> ORGANISM: Homo sapiens

134 <400> SEQUENCE: 3

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137 acaccaaggt tccaggtgct ggggagccca agtcagcctt cactcagggc tcagccatga 120
139 tttcttctct gtcccaaaac catccagaca acagaaacga gactttcagc tcagtcattt 180
141 ccctgttgaa tgaggatccc ctgtcccagg acttgccgtg gaagatggct tcaatcttca 240
143 agaactttgt cattacctat aaccggacat atgagtcaaa ggaagaagcc cgggtggcgcc 300
145 tgtccgtctt tgtcaataac atggtgcgag cacagaagat ccaggccctg gaccgtggca 360
147 cagctcagta tggagtcacc aagttcagtg atctcacaga ggaggagttc cgcactatct 420
149 acctgaatac tctcctgagg aaagagcctg gcaacaagat gaagcaagcc aagtctgttg 480
151 gtgacctcgc ccacctgaa tgggactgga ggagtaaggg ggctgtcaca aaagtcaaag 540
153 accagggcac gtgtggctcc tgctgggccc tctcagtcac aggcaatgtg gagggccagt 600
155 ggtttctcaa ccaggggacc ctgctctccc tctctgaaca ggagctcttg gactgtgaca 660
157 agatggacaa ggccctgcatg ggcggcttgc cctccaatgc ctactcggcc ataaagaatt 720
159 tgggagggct ggagacagag gatgactaca gctaccaggg tcacatgcag tcttgcaact 780
161 tctcagcaga gaaggccaaag gtctacatca atgactccgt ggagctgagc cagaacgagc 840
163 agaagctggc agcctggctg gccaaagagag gcccaatctc cgtggccatc aatgcctttg 900
165 gcatgcagtt ttaccgccac gggatctccc gccctctccg gcccctctgc agcccttggc 960
167 tcattgacca tgcggtgttg cttgtgggct acggcaaccg ctctgacgtt cccttttggg 1020
169 ccatcaagaa cagctggggc actgactggg gtgagaaggg ttactactac ttgcatcgcg 1080
171 ggtccggggc ctgtggcggtg aacaccatgg ccagctcggc ggtggtggac tgaagagggg 1140
173 ccccagctc gggacctggt gctgatcaga gtggctgctg cccagcctg acatgtgtcc 1200
175 agggccctcc ccgggaggtg cagctggcag agggaaaggg actgggtacc tcagggtgag 1260
177 cagagggcac tgggctgggg cacagcccct gctt 1294

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180 <210> SEQ ID NO: 4
181 <211> LENGTH: 338
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 4
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188 1 5 10 15
191 Phe Ser Ser Val Ile Ser Leu Leu Asn Glu Asp Pro Leu Ser Gln Asp
192 20 25 30
195 Leu Pro Val Lys Met Ala Ser Ile Phe Lys Asn Phe Val Ile Thr Tyr
196 35 40 45
199 Asn Arg Thr Tyr Glu Ser Lys Glu Glu Ala Arg Trp Arg Leu Ser Val
200 50 55 60
203 Phe Val Asn Asn Met Val Arg Ala Gln Lys Ile Gln Ala Leu Asp Arg
204 65 70 75 80
207 Gly Thr Ala Gln Tyr Gly Val Thr Lys Phe Ser Asp Leu Thr Glu Glu
208 85 90 95
211 Glu Phe Arg Thr Ile Tyr Leu Asn Thr Leu Leu Arg Lys Glu Pro Gly
212 100 105 110
215 Asn Lys Met Lys Gln Ala Lys Ser Val Gly Asp Leu Ala Pro Po Glu
216 115 120 125
219 Trp Asp Trp Arg Ser Lys Gly Ala Val Thr Lys Val Lys Asp G Gly
220 130 135 140
223 Met Cys Gly Ser Cys Trp Ala Phe Ser Val Thr Gly Asn Val G Gly
224 145 150 155 160
227 Gln Trp Phe Leu Asn Gln Gly Thr Leu Leu Ser Leu Ser Glu G Glu
228 165 170 175
231 Leu Leu Asp Cys Asp Lys Met Asp Lys Ala Cys Met Gly Gly L Pro
232 180 185 190
235 Ser Asn Ala Tyr Ser Ala Ile Lys Asn Leu Gly Gly Leu Glu TlGlu
236 195 200 205
239 Asp Asp Tyr Ser Tyr Gln Gly His Met Gln Ser Cys Asn Phe SAla
240 210 215 220
243 Glu Lys Ala Lys Val Tyr Ile Asn Asp Ser Val Glu Leu Ser GLAsn
244 225 230 235 240
247 Glu Gln Lys Leu Ala Ala Trp Leu Ala Lys Arg Gly Pro Ile Seval
248 245 250 255
251 Ala Ile Asn Ala Phe Gly Met Gln Phe Tyr Arg His Gly Ile Searg
252 260 265 270 275
255 Pro Leu Arg Pro Leu Cys Ser Pro T P Val Pro Phe Trp Ala Ile Lys
256 275 280 285 290
259 Leu Val Gly Tyr Gly Asn Arg Glu Lys Gly Tyr Tyr Tyr Leu His
260 290 300 305 310
263 Asn Ser Trp Gly Thr Asp Val Asn Thr Met Ala Ser Ser Ala Val
264 305 310 315 320
267 Arg Gly Ser Gly Ala 320 325 330 335
268
271 Val Asp
275 <210> SEQ ID

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276 <211> LENGTH: 1557
277 <212> TYPE: DNA
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283 ctggagaacc aggagctcgt cggcaaagac gggttcggca cagtgttcg ggcgcaacat      120
285 aggaagtggg gctacgatgt ggcggtcaag atcgtaaact cgaaggcgat atccagggag      180
287 gtcaaggcca tggcaagtct ggataacgaa ttcgtgttgc gcctagaagg ggttatcgag      240
289 aaggtgaact gggaccaaga tcccaagccg gctctggtga ctaaattcat ggagaacggc      300
291 tccctgtcgg ggctgctgca gtcccagtcg cctcgccctt ggccgctcct ttgccgcctg      360
293 ctgaaagaag tgggtgcttg gatgttttac ctgcacgacc agaaccgggt gtcctgcac      420
295 cgggacctca agccatccaa cgtcctgccc gacccagagc tgcacgtcaa gctggcagat      480
297 tttggcctgt ccacatttca gggaggtcca cagtcaggga cagggtccg ggagccaggg      540
299 ggcaccctgg gctacttggc cccagaactg tttgttaacg taaaccggaa ggctccaca      600
301 gccagtgcag tctacagctt cgggataccta atgtgggcag tgcctgctgg aagagaagtt      660
303 gatttgccaa ccgaaccatc actcgtgtac gaagcagtg gcaacaggca gaaccggcct      720
305 tcattggctg agctgcccc aagcgggccc gagactccc gcttagaagg actgaaggag      780
307 ctaatgcagc tctgctggag cagtgcgcc aaggacagac cctccttcca ggaatgccta      840
309 caaaaaactg atgaagtctt ccagatgggt gagaacaata tgaatgctgc tgtctccacg      900
311 gtaaaggatt tctgtctca gctcaagagc agcaatagga gattttctat cccagagtca      960
313 ggccaaggag ggacagaaat ggatggcttt aggagaacca tagaaaacca gactctcgt      1020
315 aatgatgtca tggtttctga gtggctaaac aaactgaatc tagaggagcc tcccagctct      1080
317 gttcctaaaa aatgcccag ccttaccaag aggagcaggg cacaagagga gcaggttcca      1140
319 caagcctgga cagcaggcac atcttcagat tcgatggccc aacctcccca gactccagag      1200
321 acctcaactt tcagaaacca gatgccagc cctacctcaa ctggaacacc aagtccctgga      1260
323 ccccgaggga atcagggggc tgagagacaa ggcataaact ggtcctgcag gaccccgag      1320
325 ccaaatccag taacagggcg accgctcgtt aacatataca actgctctgg ggtgcaagtt      1380
327 ggagacaaca actacttgac tatgcaacag acaactgcct tgcccacatg gggcttgga      1440
329 ccttcgggca aggggagggg cttgcagcac cccccaccag taggttcgca agaaggccct      1500
331 aaagatcctg aagcctggag caggccacag ggttggtata atcatagcgg gaaataa      1557
334 <210> SEQ ID NO: 6
335 <211> LENGTH: 519
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
339 <400> SEQUENCE: 6
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345 Ser Ile Glu Glu Leu Glu Asn Gln Glu Leu Val Gly Lys Asp Gly Phe
346 20 25 30
349 Gly Thr Val Phe Arg Ala Gln His Arg Lys Trp Gly Tyr Asp Val Ala
350 35 40 45
353 Val Lys Ile Val Asn Ser Lys Ala Ile Ser Arg Glu Val Lys Ala Met
354 50 55 60
357 Ala Ser Leu Asp Asn Glu Phe Val Leu Arg Leu Glu Gly Val Ile Glu
358 65 70 75 80
361 Lys Val Asn Trp Asp Gln Asp Pro Lys Pro Ala Leu Val Thr Lys Phe
362 85 90 95
365 Met Glu Asn Gly Ser Leu Ser Gly Leu Leu Gln Ser Gln Cys Pro Arg
366 100 105 110

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369 Pro Trp Pro Leu Leu Cys Arg Leu Leu Lys Glu Val Val Leu Gly Met
370      115      120      125
373 Phe Tyr Leu His Asp Gln Asn Pro Val Leu Leu His Arg Asp Leu Lys
374      130      135      140
377 Pro Ser Asn Val Leu Pro Asp Pro Glu Leu His Val Lys Leu Ala Asp
378 145      150      155      160
381 Phe Gly Leu Ser Thr Phe Gln Gly Gly Ser Gln Ser Gly Thr Gly Ser
382      165      170      175
385 Gly Glu Pro Gly Gly Thr Leu Gly Tyr Leu Ala Pro Glu Leu Phe Val
386      180      185      190
389 Asn Val Asn Arg Lys Ala Ser Thr Ala Ser Asp Val Tyr Ser Phe Gly
390      195      200      205
393 Ile Leu Met Trp Ala Val Leu Ala Gly Arg Glu Val Glu Leu Pro Thr
394      210      215      220
397 Glu Pro Ser Leu Val Tyr Glu Ala Val Cys Asn Arg Gln Asn Arg Pro
398 225      230      235      240
401 Ser Leu Ala Glu Leu Pro Gln Ala Gly Pro Glu Thr Pro Gly Leu Glu
402      245      250      255
405 Gly Leu Lys Glu Leu Met Gln Leu Cys Trp Ser Ser Glu Pro Lys Asp
406      260      265      270
409 Arg Pro Ser Phe Gln Glu Cys Leu Pro Lys Thr Asp Glu Val Phe Gln
410      275      280      285
413 Met Val Glu Asn Asn Met Asn Ala Ala Val Ser Thr Val Lys Asp Phe
414      290      295      300
417 Leu Ser Gln Leu Lys Ser Ser Asn Arg Arg Phe Ser Ile Pro Glu Ser
418 305      310      315      320
421 Gly Gln Gly Gly Thr Glu Met Asp Gly Phe Arg Arg Thr Ile Glu Asn
422      325      330      335
425 Gln His Ser Arg Asn Asp Val Met Val Ser Glu Trp Leu Asn Lys Leu
426      340      345      350
429 Asn Leu Glu Glu Pro Pro Ser Ser Val Pro Lys Lys Cys Pro Ser Leu
430      355      360      365
433 Thr Lys Arg Ser Arg Ala Gln Glu Glu Gln Val Pro Gln Ala Trp Thr
434      370      375      380
437 Ala Gly Thr Ser Ser Asp Ser Met Ala Gln Pro Pro Gln Thr Pro Glu
438 385      390      395      400
441 Thr Ser Thr Phe Arg Asn Gln Met Pro Ser Pro Thr Ser Thr Gly Thr
442      405      410      415
445 Pro Ser Pro Gly Pro Arg Gly Asn Gln Gly Ala Glu Arg Gln Gly Met
446      420      425      430
449 Asn Trp Ser Cys Arg Thr Pro Glu Pro Asn Pro Val Thr Gly Arg Pro
450      435      440      445
453 Leu Val Asn Ile Tyr Asn Cys Ser Gly Val Gln Val Gly Asp Asn Asn
454      450      455      460
457 Tyr Leu Thr Met Gln Gln Thr Thr Ala Leu Pro Thr Trp Gly Leu Ala
458 465      470      475      480
461 Pro Ser Gly Lys Gly Arg Gly Leu Gln His Pro Pro Pro Val Gly Ser
462      485      490      495
465 Gln Glu Gly Pro Lys Asp Pro Glu Ala Trp Ser Arg Pro Gln Gly Trp

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